

X16760 A Seq Listing.txt
SEQUENCE LISTING

<110> Allan, Barrett W.
 Davies, Julian
 Marquis, David M.
 Ondek, Brian
 Watkins, Jeffry D.

 <120> CD20 BINDING MOLECULES
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 <140> PCT/US2004/015786
 <141> 2004-05-20
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 <170> PatentIn version 3.3

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20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Ala Thr Ser Ala Leu Ala Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
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Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Leu Ser Asn Pro Pro Thr
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20 25 30

Asn Met His Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ala Ile Tyr Pro Leu Thr Gly Asp Thr Ser Tyr Asn Gln Lys Ser
50 55 60

Lys Leu Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

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 cccgggaaag gcctggagtg gatgggggct atttatccct tgacgggtga tacttcctac 180
 aatcagaagt cgaaactcca ggtcaccatc tcagccgaca agtccatcag caccgcctac 240
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val His Tyr Ile
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His Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile Tyr
35 40 45

Ala Thr Ser Gly Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65 70 75 80

Asp Val Ala Thr Tyr Tyr Cys Gln Thr Trp Thr Phe Asn Pro Pro Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
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Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Trp Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Gln Phe Asp Glu Trp Gly
100 105 110

Lys Gly Thr Thr Val Thr Val Ser Ser
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tcctgcaagg catctggata caccttcacc agctacaata tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggagcc atctatcctg gaaatgggtga tacaagctac 180
aatcagaagt ttaaattggag agtcaccatg accagggaca cgtccacgag cacagtctac 240
atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagatcgact 300
tattacggcg gtgactggca gttcgacgag tggggcaaag ggaccacggt caccgtctcc 360
tca 363

X16760 A Seq Listing.txt

<210> 67
 <211> 213
 <212> PRT
 <213> artificial

<220>
 <223> Synthetic construct

<220>
 <221> MISC_FEATURE
 <222> (1)..(213)
 <223> AME 33 complete light chain

<400> 67

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Pro Tyr Ile
 20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
 35 40 45

Ala Thr Ser Ala Leu Ala Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Leu Ser Asn Pro Pro Thr
 85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190

X16760 A Seq Listing.txt

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205

Asn Arg Gly Glu Cys
 210

<210> 68
 <211> 642
 <212> DNA
 <213> artificial

<220>
 <223> Synthetic construct

<220>
 <221> misc_feature
 <222> (1)..(642)
 <223> AME 33 complete light chain

<400> 68
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 caggctccca ggctcctcat ctatgccaca tccgctctgg cttctggcat cccagacagg 180
 ttcagtggca gtgggtctgg gacagacttc actctcacca tcagcagact ggagcctgaa 240
 gattttgcag tgtattactg tcagcagtgg ctgagtaacc caccacttt tggccagggg 300
 accaagctgg agatcaaacg aactgtggct gcaccatctg tcttcattctt cccgccatct 360
 gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc 420
 agagaggcca aagtacagtg gaagggtggat aacgccctcc aatcgggtaa ctcccaggag 480
 agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg 540
 agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg 600
 agctcgcccc tcacaaagag cttcaacagg ggagagtgtt ag 642

<210> 69
 <211> 451
 <212> PRT
 <213> artificial

<220>
 <223> Synthetic construct

<220>
 <221> MISC_FEATURE
 <222> (1)..(451)
 <223> AME 33 complete heavy chain

<400> 69

X16760 A Seq Listing.txt

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15
 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Arg Thr Phe Thr Ser Tyr
 20 25 30
 Asn Met His Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Ala Ile Tyr Pro Leu Thr Gly Asp Thr Ser Tyr Asn Gln Lys Ser
 50 55 60
 Lys Leu Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg Ser Thr Tyr Val Gly Gly Asp Trp Gln Phe Asp Val Trp Gly
 100 105 110
 Lys Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 130 135 140
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
 210 215 220
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 225 230 235 240
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255

X16760 A Seq Listing.txt

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 70
<211> 1356
<212> DNA
<213> artificial

<220>
<223> synthetic construct

<220>

X16760 A Seq Listing.txt

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<221> misc_feature
<222> (1)..(1356)
<223> AME 33 complete heavy chain

<400> 70
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tcctgtaagg gttctggccg tacatttacc agttacaata tgcactgggt gcgccagatg      120
cccgggaaag gcctggagtg gatgggggct atttatccct tgacgggtga tacttcctac      180
aatcagaagt cgaaactcca ggtcaccatc tcagccgaca agtccatcag caccgcctac      240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagatcgact      300
tacgtgggcg gtgactggca gttcgaatgc tggggcaagg ggaccacggg caccgtctcc      360
tcagcctcca ccaaggggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct      420
gggggacacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacgggtg      480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggtgtg cctacagtcc      540
tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcacccag      600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaagggtgag      660
cccaaattct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg      720
ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca ccctcatgat ctcccggacc      780
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac      840
tggtacgtgg acggcgtgga ggtgcataat gccaaagaaa agccgcggga ggagcagtac      900
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc      960
aaggagtaca agtgcaagggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc     1020
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggac     1080
gagctgacca agaaccagggt cagcctgacc tgcttggtca aaggcttcta tcccagcgac     1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc     1200
gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg     1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgatg aggctctgca caaccactac     1320
acgcagaaga gcctctccct gtctccgggt aaatga                                  1356

<210> 71
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(23)
<223> FRL1 VkIII (A27)(DPK22)

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X16760 A Seq Listing.txt

<400> 71

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys
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<210> 72
<211> 15
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(15)
<223> FRL2 VKIII (A27)(DPK22)

<400> 72

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 73
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(32)
<223> FRL3 VKIII (A27)(DPK22)

<400> 73

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
20 25 30

<210> 74
<211> 10
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(10)
<223> FRL4 VKIII (A27)(DPK22)

<400> 74

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
1 5 10

X16760 A Seq Listing.txt

<210> 75
 <211> 69
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(69)
 <223> FRL1 VkIII (A27)(DPK22)

<400> 75
 gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcctgc 69

<210> 76
 <211> 45
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(45)
 <223> FRL2 VkIII (A27)(DPK22)

<400> 76
 tggtaccagc agaaacctgg ccaggctccc aggctcctca tctat 45

<210> 77
 <211> 96
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(96)
 <223> FRL3 VkIII (A27)(DPK22)

<400> 77
 ggcattccag acaggttcag tggcagtggg tctgggacag acttcactct caccatcagc 60
 agactggagc ctgaagattt tgcagtgtat tactgt 96

<210> 78
 <211> 30
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(30)
 <223> FRL4 VkIII (A27)(DPK22)

<400> 78

tttggccagg ggaccaagct ggagatcaaa

30

<210> 79
 <211> 25
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(25)
 <223> FRH1 VH5-51 (DPK-73)

<400> 79

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser
 20 25

<210> 80
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> FRH2 VH5-51 (DP-73)

<400> 80

Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
 1 5 10

<210> 81
 <211> 32
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(32)
 <223> FRH3 VH5-51 (DP-73)

<400> 81

Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln
 1 5 10 15

Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg
 20 25 30

<210> 82

x16760 A Seq Listing.txt

<211> 11
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(11)
<223> FRH4 VH5-51 (DP-73)

<400> 82

Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 83
<211> 75
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(75)
<223> FRH1 VH5-51 (DP-73)

<400> 83
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60
tcctgtaagg gttct 75

<210> 84
<211> 96
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(96)
<223> FRH2 VH5-51 (DP-73)

<400> 84
tgggtgcgcc agatgcccgg gaaaggcctg gagtggatgg ggcagggtcac catctcagcc 60
gacaagtcca tcagcacccgc ctacctgcag tggagc 96

<210> 85
<211> 42
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(42)
<223> FRH3 VH5-51 (DP-73)

<400> 85
agcctgaagg cctcggacac cgccatgtat tactgtgcga ga 42

x16760 A Seq Listing.txt

<210> 86
 <211> 33
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(33)
 <223> FRH4 VH5-51 (DP-73)

<400> 86
 tggggcaagg ggaccacggt caccgtctcc tca

33

<210> 87
 <211> 23
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(23)
 <223> FRL1 Vki (DPK4)(A20)

<400> 87

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys
 20

<210> 88
 <211> 15
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(15)
 <223> FRL2 Vki (DPK4)(A20)

<400> 88

Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile Tyr
 1 5 10 15

<210> 89
 <211> 32
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE

x16760 A Seq Listing.txt

<222> (1)..(32)

<223> FRL3 vki (DPK4)(A20)

<400> 89

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys
20 25 30

<210> 90

<211> 10

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(10)

<223> FRL4 vki (DPK4)(A20)

<400> 90

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 91

<211> 69

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(69)

<223> FRL1 vki (DPK4)(A20)

<400> 91

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgc 69

<210> 92

<211> 45

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(45)

<223> FRL2 vki (DPK4)(A20)

<400> 92

tggtaccagc agaaaccagg gaaagttcct aagctcttga tctat 45

<210> 93

x16760 A Seq Listing.txt

<211> 96
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(96)
 <223> FRL3 vki (DPK4)(A20)

<400> 93
 ggggtcccat ctcggttcag tggcagtgga tctgggacag atttcactct caccatcagc 60
 agcctgcagc ctgaagatgt tgccacttat tactgc 96

<210> 94
 <211> 30
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(30)
 <223> FRL4 vki (DPK4)(A20)

<400> 94
 ttcggcggag ggaccaaggt ggagatcaaa 30

<210> 95
 <211> 25
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(25)
 <223> FRH1 vki (DP7/21-2)

<400> 95
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser
 20 25

<210> 96
 <211> 14
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> FRH2 vki (DP7/21-2)

X16760 A Seq Listing.txt

<400> 96

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 5 10

<210> 97

<211> 32

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(32)

<223> FRH3 vKI (DP7/21-2)

<400> 97

Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 98

<211> 11

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(11)

<223> FRH4 vKI (DP7/21-2)

<400> 98

Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 99

<211> 75

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(75)

<223> FRH1 vKI (DP7/21-2)

<400> 99

cagggtgcagc tgggtgcagtc tgggtgctgaa gtgaagaagc ctggggcctc agtgaagggtg 60
tcctgcaagg catct 75

<210> 100

<211> 40

x16760 A Seq Listing.txt

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(40)
<223> FRH2 vki (DP7/21-2)

<400> 100
ggtgcgacag gcccctggac aagggcttga gtggatggga 40

<210> 101
<211> 96
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(96)
<223> FRH3 vki (DP7/21-2)

<400> 101
agagtcacca tgaccaggga cacgtccacg agcacagtct acatggagct gagcagcctg 60
agatctgagg acacggccgt gtattactgt gcgaga 96

<210> 102
<211> 33
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(33)
<223> FRH4 vki (DP7/21-2)

<400> 102
tggggcaaag ggaccacggt caccgtctcc tca 33